

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/530, 217 A  
Source: PCT  
Date Processed by STIC: 05/15/2006

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 05/15/2006

PATENT APPLICATION: US/10/530,217A

TIME: 10:00:16

Input Set : A:\082368-003910US - Substitute Sequence Listing.txt

Output Set: N:\CRF4\05152006\J530217A.raw

4 <110> APPLICANT: Nakamura, Yusuke  
 5 Katagiri, Toyomasa  
 7 <120> TITLE OF INVENTION: GENES AND POLYPEPTIDES RELATING TO HUMAN  
 8 MYELOID LEUKEMIA  
 10 <130> FILE REFERENCE: 082368-003910US  
 12 <140> CURRENT APPLICATION NUMBER: 10/530,217A  
 C--> 13 <141> **CURRENT FILING DATE: 2005-03-30**  
 15 <150> PRIOR APPLICATION NUMBER: PCT/JP03/09589  
 16 <151> PRIOR FILING DATE: 2003-07-29  
 18 <150> PRIOR APPLICATION NUMBER: US 60/414,867  
 19 <151> PRIOR FILING DATE: 2002-09-30  
 21 <160> NUMBER OF SEQ ID NOS: 16  
 23 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 25 <210> SEQ ID NO: 1  
 26 <211> LENGTH: 22  
 27 <212> TYPE: DNA  
 28 <213> ORGANISM: Artificial Sequence  
 30 <220> FEATURE:  
 31 <223> OTHER INFORMATION: Artificially synthesized primer sequence for  
 32 RT-PCR  
 34 <400> SEQUENCE: 1  
 35 gtgctcttcc tcttcacctt tg 22  
 37 <210> SEQ ID NO: 2  
 38 <211> LENGTH: 23  
 39 <212> TYPE: DNA  
 40 <213> ORGANISM: Artificial Sequence  
 42 <220> FEATURE:  
 43 <223> OTHER INFORMATION: Artificially synthesized primer sequence for  
 44 RT-PCR  
 46 <400> SEQUENCE: 2  
 47 ggtggtcgtc aagaaacaag tta 23  
 49 <210> SEQ ID NO: 3  
 50 <211> LENGTH: 23  
 51 <212> TYPE: DNA  
 52 <213> ORGANISM: Artificial Sequence  
 54 <220> FEATURE:  
 55 <223> OTHER INFORMATION: Artificially synthesized primer sequence for  
 56 RT-PCR  
 58 <400> SEQUENCE: 3  
 59 catccacgaa actaccttca act 23  
 61 <210> SEQ ID NO: 4  
 62 <211> LENGTH: 23  
 63 <212> TYPE: DNA

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64 <213> ORGANISM: Artificial Sequence
66 <220> FEATURE:
67 <223> OTHER INFORMATION: Artificially synthesized primer sequence for
68     RT-PCR
70 <400> SEQUENCE: 4
71 tctccttaga gagaagtggg gtg                23
73 <210> SEQ ID NO: 5
74 <211> LENGTH: 22
75 <212> TYPE: DNA
76 <213> ORGANISM: Artificial Sequence
78 <220> FEATURE:
79 <223> OTHER INFORMATION: Artificially synthesized primer sequence for
80     RT-PCR
82 <400> SEQUENCE: 5
83 gtgctcttcc tcttcacctt tg                22
85 <210> SEQ ID NO: 6
86 <211> LENGTH: 23
87 <212> TYPE: DNA
88 <213> ORGANISM: Artificial Sequence
90 <220> FEATURE:
91 <223> OTHER INFORMATION: Artificially synthesized primer sequence for
92     RT-PCR
94 <400> SEQUENCE: 6
95 ggtggtcgtc aagaaacaag tta                23
97 <210> SEQ ID NO: 7
98 <211> LENGTH: 23
99 <212> TYPE: DNA
100 <213> ORGANISM: Artificial Sequence
102 <220> FEATURE:
103 <223> OTHER INFORMATION: Artificially synthesized primer sequence for
104     RT-PCR
106 <400> SEQUENCE: 7
107 gacaactcac tcaagattgt cag                23
109 <210> SEQ ID NO: 8
110 <211> LENGTH: 20
111 <212> TYPE: DNA
112 <213> ORGANISM: Artificial Sequence
114 <220> FEATURE:
115 <223> OTHER INFORMATION: Artificially synthesized primer sequence for
116     RT-PCR
119 <400> SEQUENCE: 8
120 gatccacgac ggacacattg                20
122 <210> SEQ ID NO: 9
123 <211> LENGTH: 28
124 <212> TYPE: DNA
125 <213> ORGANISM: Artificial Sequence
127 <220> FEATURE:
128 <223> OTHER INFORMATION: Artificially synthesized primer sequence for
129     RT-PCR

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131 <400> SEQUENCE: 9
132 cgggaattccg atgagtgagg cccgcagg                28
134 <210> SEQ ID NO: 10
135 <211> LENGTH: 29
136 <212> TYPE: DNA
137 <213> ORGANISM: Artificial Sequence
139 <220> FEATURE:
140 <223> OTHER INFORMATION: Artificially synthesized primer sequence for
141     RT-PCR
143 <400> SEQUENCE: 10
144 ggggtacccc agtggagctg agcgtccag                29
146 <210> SEQ ID NO: 11
147 <211> LENGTH: 18
148 <212> TYPE: DNA
149 <213> ORGANISM: Artificial Sequence
151 <220> FEATURE:
152 <223> OTHER INFORMATION: Artificially synthesized S-oligonucleotide
153     sequence for antisense
155 <400> SEQUENCE: 11
156 ctgtgtgatg gacgtctg                            18
158 <210> SEQ ID NO: 12
159 <211> LENGTH: 18
160 <212> TYPE: DNA
161 <213> ORGANISM: Artificial Sequence
163 <220> FEATURE:
164 <223> OTHER INFORMATION: Artificially synthesized S-oligonucleotide
165     sequence for antisense
167 <400> SEQUENCE: 12
168 gtctgcaggt agtgtgtc                            18
170 <210> SEQ ID NO: 13
171 <211> LENGTH: 19
172 <212> TYPE: DNA
173 <213> ORGANISM: Artificial Sequence
175 <220> FEATURE:
176 <223> OTHER INFORMATION: Target sequence for siRNA
178 <400> SEQUENCE: 13
179 gtacgtgcag caggagaac                            19
181 <210> SEQ ID NO: 14
182 <211> LENGTH: 19
183 <212> TYPE: DNA
184 <213> ORGANISM: Artificial Sequence
186 <220> FEATURE:
187 <223> OTHER INFORMATION: Target sequence for siRNA
189 <400> SEQUENCE: 14
190 gaagcagcac gacttcttc                            19
192 <210> SEQ ID NO: 15
193 <211> LENGTH: 2958
194 <212> TYPE: DNA
195 <213> ORGANISM: Homo sapiens

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197 <220> FEATURE:
198 <221> NAME/KEY: CDS
199 <222> LOCATION: (111)...(2678)
201 <400> SEQUENCE: 15
202 ctcggcgcgcg gcgcctctccc ggccagcgcg gcgcagccct cctccccggc gccctcagga 60
203 cccccccagag acccccggcg gcggcagcct gccttgctct gccaggaacc atg agt 116
204                                     Met Ser
205                                     1
207 gag gcc cgc agg gac agc acg agc agc ctg cag cgc aag aag cca ccc 164
208 Glu Ala Arg Arg Asp Ser Thr Ser Ser Leu Gln Arg Lys Lys Pro Pro
209         5                10                15
211 tgg cta aag ctg gac att ccc tct gcg gtg ccc ctg acg gca gaa gag 212
212 Trp Leu Lys Leu Asp Ile Pro Ser Ala Val Pro Leu Thr Ala Glu Glu
213         20                25                30
215 ccc agc ttc ctg cag ccc ctg agg cga cag gct ttc ctg agg agt gtg 260
216 Pro Ser Phe Leu Gln Pro Leu Arg Arg Gln Ala Phe Leu Arg Ser Val
217         35                40                45                50
219 agt atg cca gcc gag aca gcc cac atc tct tca ccc cac cat gag ctc 308
220 Ser Met Pro Ala Glu Thr Ala His Ile Ser Ser Pro His His Glu Leu
221         55                60                65
223 cgg cgg ccg gtg ctg caa cgc cag acg tcc atc aca cag acc atc cgc 356
224 Arg Arg Pro Val Leu Gln Arg Gln Thr Ser Ile Thr Gln Thr Ile Arg
225         70                75                80
227 agg ggg acc gcc gac tgg ttt gga gtg agc aag gac agt gac agc acc 404
228 Arg Gly Thr Ala Asp Trp Phe Gly Val Ser Lys Asp Ser Asp Ser Thr
229         85                90                95
231 cag aaa tgg cag cgc aag agc atc cgt cac tgc agc cag cgc tac ggg 452
232 Gln Lys Trp Gln Arg Lys Ser Ile Arg His Cys Ser Gln Arg Tyr Gly
233         100               105               110
235 aag ctg aag ccc cag gtc ctc cgg gag ctg gac ctg ccc agc cag gac 500
236 Lys Leu Lys Pro Gln Val Leu Arg Glu Leu Asp Leu Pro Ser Gln Asp
237 115                120                125                130
239 aac gtg tcg ctg acc agc acc gag acg cca ccc cca ctc tac gtg ggg 548
240 Asn Val Ser Leu Thr Ser Thr Glu Thr Pro Pro Pro Leu Tyr Val Gly
241         135               140               145
243 cca tgc cag ctg ggc atg cag aag atc ata gac ccc ctg gcc cgt ggc 596
244 Pro Cys Gln Leu Gly Met Gln Lys Ile Ile Asp Pro Leu Ala Arg Gly
245         150               155               160
247 cgt gcc ttc cgt gtg gca gat gac act gcg gaa ggc ctg agt gcc cca 644
248 Arg Ala Phe Arg Val Ala Asp Asp Thr Ala Glu Gly Leu Ser Ala Pro
249         165               170               175
251 cac act ccc gtc acg ccg ggt gct gcc tcc ctc tgc tcc ttc tcc agc 692
252 His Thr Pro Val Thr Pro Gly Ala Ala Ser Leu Cys Ser Phe Ser Ser
253         180               185               190
255 tcc cgc tca ggt ttc cac cgg ctc ccg cgg cgg cgc aag cga gag tcg 740
256 Ser Arg Ser Gly Phe His Arg Leu Pro Arg Arg Arg Lys Arg Glu Ser
257 195                200                205                210
259 gtg gcc aag atg agc ttc cgg gcg gcc gca gcg ctg atg aaa ggc cgc 788
260 Val Ala Lys Met Ser Phe Arg Ala Ala Ala Ala Leu Met Lys Gly Arg

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261		215		220		225		
263	tcc gtt agg gat ggc acc ttt cgc cgg gca cgg cgt cga agc ttc act	836						
264	Ser Val Arg Asp Gly Thr Phe Arg Arg Ala Arg Arg Ser Phe Thr							
265		230		235		240		
267	cca gct agc ttt ctg gag gag gac aca act gat ttc ccc gat gag ctg	884						
268	Pro Ala Ser Phe Leu Glu Glu Asp Thr Thr Asp Phe Pro Asp Glu Leu							
269		245		250		255		
271	gac aca tcc ttc ttt gcc cgg gaa ggt atc ctc cat gaa gag ctg tcc	932						
272	Asp Thr Ser Phe Phe Ala Arg Glu Gly Ile Leu His Glu Glu Leu Ser							
273		260		265		270		
275	aca tac ccg gat gaa gtt ttc gag tcc cca tcg gag gca gcg cta aag	980						
276	Thr Tyr Pro Asp Glu Val Phe Glu Ser Pro Ser Glu Ala Ala Leu Lys							
277		275		280		285		290
279	gac tgg gag aag gca ccg gag cag gcg gac ctc acc ggc ggg gcc ctg	1028						
280	Asp Trp Glu Lys Ala Pro Glu Gln Ala Asp Leu Thr Gly Gly Ala Leu							
281		295		300		305		
283	gac cgc agc gag ctt gag cgc agc cac ctg atg ctg ccc ttg gag cga	1076						
284	Asp Arg Ser Glu Leu Glu Arg Ser His Leu Met Leu Pro Leu Glu Arg							
285		310		315		320		
287	ggc tgg cgg aag cag aag gag ggc gcc gca gcc ccg cag ccc aag gtg	1124						
288	Gly Trp Arg Lys Gln Lys Glu Gly Ala Ala Ala Pro Gln Pro Lys Val							
289		325		330		335		
291	cgg ctc cga cag gag gtg gtg agc acc gcg ggg ccg cga cgg ggc cag	1172						
292	Arg Leu Arg Gln Glu Val Val Ser Thr Ala Gly Pro Arg Arg Gly Gln							
293		340		345		350		
295	cgt atc gcg gtg ccg gtg cgc aag ctc ttc gcc cgg gag aag cgg ccg	1220						
296	Arg Ile Ala Val Pro Val Arg Lys Leu Phe Ala Arg Glu Lys Arg Pro							
297		355		360		365		370
299	tat ggg ctg ggc atg gtg gga cgg ctc acc aac cgc acc tac cgc aag	1268						
300	Tyr Gly Leu Gly Met Val Gly Arg Leu Thr Asn Arg Thr Tyr Arg Lys							
301		375		380		385		
303	cgc atc gac agc ttc gtc aag cgc cag atc gag gac atg gac gac cac	1316						
304	Arg Ile Asp Ser Phe Val Lys Arg Gln Ile Glu Asp Met Asp Asp His							
305		390		395		400		
307	agg ccc ttc ttc acc tac tgg ctt acc ttc gtg cac tcg ctc gtc acc	1364						
308	Arg Pro Phe Phe Thr Tyr Trp Leu Thr Phe Val His Ser Leu Val Thr							
309		405		410		415		
311	atc cta gcc gtg tgc atc tat ggc atc gcg ccc gtg ggc ttc tcg cag	1412						
313	Ile Leu Ala Val Cys Ile Tyr Gly Ile Ala Pro Val Gly Phe Ser Gln							
314		420		425		430		
316	cat gag acg gtg gac tcg gtg ctg cgg aac cgc ggg gtc tac gag aac	1460						
317	His Glu Thr Val Asp Ser Val Leu Arg Asn Arg Gly Val Tyr Glu Asn							
318		435		440		445		450
320	gtc aag tac gtg cag cag gag aac ttc tgg atc ggg ccc agc tcg gag	1508						
321	Val Lys Tyr Val Gln Gln Glu Asn Phe Trp Ile Gly Pro Ser Ser Glu							
322		455		460		465		
324	gcc ctc atc cac ctg ggc gcc aag ttt tcg ccc tgc atg cgc cag gac	1556						
325	Ala Leu Ile His Leu Gly Ala Lys Phe Ser Pro Cys Met Arg Gln Asp							
326		470		475		480		

**VERIFICATION SUMMARY**

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L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date